



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/492,971  
Source: 1600  
Date Processed by STIC: 6-9-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

09/492,971

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence  
(2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/492,971

DATE: 06/09/2004

TIME: 16:16:32

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\06092004\I492971.raw

3 <110> APPLICANT: Vogel et al., Tikva  
 5 <120> TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND USES AND METHODS OF PRODUCING SAME  
 7 <130> FILE REFERENCE: 25775-CZ-AZ-A  
 9 <140> CURRENT APPLICATION NUMBER: US 09/492,971  
 10 <141> CURRENT FILING DATE: 2000-01-27  
 12 <160> NUMBER OF SEQ ID NOS: 38  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 11  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Synthetic Probe *See item 10 on error summary report*  
 21 <400> SEQUENCE: 1  
 22 ctgtttaagc a 11  
 25 <210> SEQ ID NO: 2  
 26 <211> LENGTH: 15  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Synthetic Probe  
 30 <400> SEQUENCE: 2  
 31 gacaaattcg tctag 15  
 34 <210> SEQ ID NO: 3  
 35 <211> LENGTH: 41  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Synthetic Probe  
 39 <400> SEQUENCE: 3  
 40 tgagaagtgt ttgatcatg ctgctgggac ttcctatgtg g 41  
 43 <210> SEQ ID NO: 4  
 44 <211> LENGTH: 43  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Synthetic Probe  
 48 <400> SEQUENCE: 4  
 49 tccgaccaga taggaagtcc cagcagcatg atcaaaacac ttc 43  
 52 <210> SEQ ID NO: 5  
 53 <211> LENGTH: 45  
 54 <212> TYPE: DNA  
 55 <213> ORGANISM: Synthetic Probe  
 57 <400> SEQUENCE: 5  
 58 tcggagaaaac gtgggagaag ccctaccaag gctggatgat ggtag 45  
 61 <210> SEQ ID NO: 6  
 62 <211> LENGTH: 45  
 63 <212> TYPE: DNA  
 64 <213> ORGANISM: Synthetic Probe  
 66 <400> SEQUENCE: 6  
 67 acaatctacc atcatccagc cttggtaggg cttctccac gtttc 45

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Input Set : A:\PTO.FG.txt

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70 <210> SEQ ID NO: 7
71 <211> LENGTH: 45
72 <212> TYPE: DNA
73 <213> ORGANISM: Synthetic Probe
75 <400> SEQUENCE: 7
76 attgtacttg cctgggagaa ggcagcggac gcatcacttg cactt      45
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 44
81 <212> TYPE: DNA
82 <213> ORGANISM: Synthetic Probe  some error
84 <400> SEQUENCE: 8
85 ctagaactgc aagtgatgcg tccgctgcct tctcccaggc aagt      44
88 <210> SEQ ID NO: 9
89 <211> LENGTH: 38
90 <212> TYPE: DNA
91 <213> ORGANISM: Synthetic Probe
93 <400> SEQUENCE: 9
94 cctcctgttt ctccgtaagt gatcctgtaa tatctcac      38
97 <210> SEQ ID NO: 10
98 <211> LENGTH: 33
99 <212> TYPE: DNA
100 <213> ORGANISM: Synthetic Probe
102 <400> SEQUENCE: 10
103 gaatcaagac ctgttttctg tcttctctta aga      33
106 <210> SEQ ID NO: 11
107 <211> LENGTH: 40
108 <212> TYPE: DNA
109 <213> ORGANISM: Synthetic Probe
111 <400> SEQUENCE: 11
112 ccaggtcctt cggaacatca gaaactgttg attggtggcc      40
115 <210> SEQ ID NO: 12
116 <211> LENGTH: 36
117 <212> TYPE: DNA
118 <213> ORGANISM: Synthetic Probe
120 <400> SEQUENCE: 12
121 aattctgtga cacagtggcc atagggaggc tggggg      36
124 <210> SEQ ID NO: 13
125 <211> LENGTH: 42
126 <212> TYPE: DNA
127 <213> ORGANISM: Synthetic Probe
129 <400> SEQUENCE: 13
130 catgaccctt tcattggttg tgcagatttc ctcgtagggca gc      42
133 <210> SEQ ID NO: 14
134 <211> LENGTH: 14
135 <212> TYPE: DNA
136 <213> ORGANISM: Synthetic Probe
138 <400> SEQUENCE: 14
139 ctgtttaata agca      14
142 <210> SEQ ID NO: 15

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## RAW SEQUENCE LISTING

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143 <211> LENGTH: 2327
144 <212> TYPE: PRT
145 <213> ORGANISM: Synthetic Probe, same error
147 <400> SEQUENCE: 15
149 Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala
150 1 5 10 15
153 Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln
154 20 25 30
157 Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys
158 35 40 45
161 Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu
162 50 55 60
165 Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val
166 65 70 75 80
169 Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr
170 85 90 95
173 Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg
174 100 105 110
177 Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg
178 115 120 125
181 Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn
182 130 135 140
185 Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp
186 145 150 155 160
189 His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro
190 165 170 175
193 Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser
194 180 185 190
197 Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr
198 195 200 205
201 Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg
202 210 215 220
205 Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp
206 225 230 235 240
209 Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly
210 245 250 255
213 Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro
214 260 265 270
217 Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr
218 275 280 285
221 Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu
222 290 295 300
225 Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr
226 305 310 315 320
229 Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro Phe
230 325 330 335
233 Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln
234 340 345 350
237 Asp Gly His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln

```

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```

238          355          360          365
241 Lys Tyr Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly
242          370          375          380
245 Gly Asn Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn
246 385          390          395          400
249 His Asn Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys
250          405          410          415
253 Trp Cys Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe
254          420          425          430
257 Cys Pro Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val
258          435          440          445
261 Met Tyr Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His
262          450          455          460
265 Met Met Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys
266 465          470          475          480
269 Ile Ala Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr
270          485          490          495
273 Tyr Asn Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met
274          500          505          510
277 Leu Asn Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp
278          515          520          525
281 Pro Val Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile
282          530          535          540
285 Gly Asp Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr
286 545          550          555          560
289 Cys Tyr Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr
290          565          570          575
293 Tyr Pro Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro
294          580          585          590
297 Ser Gln Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser
298          595          600          605
301 His Ile Ser Lys Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly
302          610          615          620
305 Arg Trp Lys Glu Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile
306 625          630          635          640
309 Lys Gly Leu Lys Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile
310          645          650          655
313 Gln Gln Tyr Gly His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr
314          660          665          670
317 Ser Thr Ser Thr Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr
318          675          680          685
321 Pro Phe Ser Pro Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr
322          690          695          700
325 Ala Ser Ser Phe Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser
326 705          710          715          720
329 Gly Phe Arg Val Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln
330          725          730          735
333 Tyr Leu Asp Leu Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu
334          740          745          750

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```

337 Leu Pro Gly Arg Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp
338      755      760      765
341 Gly Glu Gln Ser Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp
342      770      775      780
345 Ala Pro Pro Asp Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val
346 785      790      795      800
349 Val Arg Trp Ser Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val
350      805      810      815
353 Tyr Ser Pro Ser Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu
354      820      825      830
357 Thr Ala Asn Ser Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr
358      835      840      845
361 Asn Ile Thr Ile Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val
362      850      855      860
365 Val Ile Gln Gln Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro
366 865      870      875      880
369 Ser Pro Arg Asp Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr
370      885      890      895
373 Ile Met Trp Thr Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp
374      900      905      910
377 Val Ile Pro Val Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile
378      915      920      925
381 Ser Arg Asn Thr Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr
382      930      935      940
385 Tyr Tyr Phe Lys Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro
386 945      950      955      960
389 Leu Thr Ala Gln Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln
390      965      970      975
393 Phe Val Asn Glu Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro
394      980      985      990
397 Arg Ala Gln Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg
398      995      1000      1005
401 Gly Gln Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr
402      1010      1015      1020
405 Pro Leu Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu
406      1025      1030      1035
409 Val Ala Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val
410      1040      1045      1050
413 Phe Thr Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr
414      1055      1060      1065
417 Glu Val Thr Glu Thr Thr Ile Val Ile Thr Trp Thr Pro Ala Pro
418      1070      1075      1080
421 Arg Ile Gly Phe Lys Leu Gly Val Arg Pro Ser Gln Gly Gly Glu
422      1085      1090      1095
425 Ala Pro Arg Glu Val Thr Ser Asp Ser Gly Ser Ile Val Val Ser
426      1100      1105      1110
429 Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr Thr Ile Gln Val Leu
430      1115      1120      1125
433 Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val Asn Lys Val Val

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5



**VERIFICATION SUMMARY**

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